

SEQUENCE LISTING

<110> Walke, D. Wade
Scoville, John
Turner, C. Alexander Jr.

<120> Novel Human Alpha Macroglobulin Family Proteins and Polynucleotides
Encoding the Same

<130> LEX-0282-USA

<150> US 60/255,566

<151> 2000-12-14

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4338

<212> DNA

<213> homo sapiens

<400> 1

atgcagggcc	caccgctcct	gaccgcccgc	cacctcctct	gcgtgtgcac	cgccgcgctg	60
gccgtggctc	ccgggcctcg	gtttctggtg	acagccccag	ggatcatcag	gcccggagga	120
aatgtgacta	ttgggggtgga	gcttctggaa	cactgccctt	cacaggtgac	tgtgaaggcg	180
gagctgctca	agacagcatc	aaacctcact	gtctctgtcc	tggaagcaga	aggagtcttt	240
gaaaaaggct	cttttaagac	acttactctt	ccatcactac	ctctgaacag	tgcagatgag	300
atztatgagc	tacgtgtaac	cggacgtacc	caggatgaga	ttttattctc	taatagtacc	360
cgcttatcat	ttgagaccaa	gagaatatct	gtcttcattc	aaacagacaa	ggccttatac	420
aagccaaagc	aagaagtgaa	gtttcgcatt	gttacactct	tctcagattt	taagccttac	480
aaaacctctt	taaacattct	cattaaggac	cccaaataca	atgtgatcca	acagtgggtg	540
tcacaacaaa	gtgatcttgg	agtcatttcc	aaaacttttc	agctatcttc	ccatccaata	600
cttggtgact	ggctctattca	agttcaagt	aatgaccaga	catattatca	atcatttcag	660
gtttcagaat	atgtattacc	aaaatttgaa	gtgactttgc	agacaccatt	atattgttct	720
atgaattcta	agcattttaa	tggtaccatc	acggcaaagt	atacatatgg	gaagccagt	780
aaaggagacy	taacgcttac	atttttacct	ttatcctttt	ggggaaagaa	gaaaaatatt	840
acaaaaacat	ttaagataaa	tggatctgca	aacttctctt	ttaatgatga	agagatgaaa	900
aatgtaatgg	attcttcaaa	tggactttct	gaatacctgg	atctatcttc	ccctggacca	960
gtagaaattt	taaccacagt	gacagaatca	gttacaggta	tttcaagaaa	tgtgaagcact	1020
aatgtgttct	tcaagcaaca	tgattacatc	attgagtttt	ttgattatac	tactgtcttg	1080
aagccatctc	tcaacttcac	agccactgtg	aaggtaactc	gtgctgatgg	caaccaactg	1140
actcttgaag	aaagaagaaa	taatgtagtc	ataacagtga	cacagagaaa	ctatactgag	1200
tactggagcg	gatctaacag	tggaaatcag	aaaatggaag	ctgttcagaa	aataaattat	1260
actgtccccc	aaagtggaac	ttttaagatt	gaattcccaa	tccctggagga	ttccagttag	1320
ctacagttga	aggcctatct	ccttggtagt	aaaagtagca	tggcagttca	tagtctgttt	1380
aagtctccta	gtaagacata	catccaacta	aaaacaagag	atgaaaatat	aaaggtggga	1440
tcgccttttg	agttggtggt	tagtggcaac	aaacgattga	aggagttaag	ctatatggta	1500
gtatccaggg	gacagttggt	ggctgtagga	aaacaaaatt	caacaatggt	ctctttaaca	1560
ccagaaaatt	cttggactcc	aaaagcctgt	gtaatttgtt	attatattga	agatgatggg	1620
gaaattataa	gtgatgttct	aaaaattcct	gttcagcttg	tttttaaaaa	taagataaag	1680
ctatatggga	gtaaagtgaa	agctgaacca	tctgagaaag	tctctcttag	gatctctgtg	1740
acacagcctg	actccatagt	tgggattgta	gctgttgaca	aaagtgtgaa	tctgatgaat	1800
gcctctaatt	atattacaat	ggaaaatgtg	gtccatgagt	tggaacttta	taacacagga	1860
tattatttag	gcatgttcat	gaattctttt	gcagtccttc	aggaatgtgg	actctgggta	1920

Thr	Ala	Ser	Asn	Leu	Thr	Val	Ser	Val	Leu	Glu	Ala	Glu	Gly	Val	Phe
65					70					75					80
Glu	Lys	Gly	Ser	Phe	Lys	Thr	Leu	Thr	Leu	Pro	Ser	Leu	Pro	Leu	Asn
				85					90					95	
Ser	Ala	Asp	Glu	Ile	Tyr	Glu	Leu	Arg	Val	Thr	Gly	Arg	Thr	Gln	Asp
			100					105					110		
Glu	Ile	Leu	Phe	Ser	Asn	Ser	Thr	Arg	Leu	Ser	Phe	Glu	Thr	Lys	Arg
		115					120					125			
Ile	Ser	Val	Phe	Ile	Gln	Thr	Asp	Lys	Ala	Leu	Tyr	Lys	Pro	Lys	Gln
	130					135					140				
Glu	Val	Lys	Phe	Arg	Ile	Val	Thr	Leu	Phe	Ser	Asp	Phe	Lys	Pro	Tyr
145					150					155					160
Lys	Thr	Ser	Leu	Asn	Ile	Leu	Ile	Lys	Asp	Pro	Lys	Ser	Asn	Leu	Ile
				165					170					175	
Gln	Gln	Trp	Leu	Ser	Gln	Gln	Ser	Asp	Leu	Gly	Val	Ile	Ser	Lys	Thr
			180					185					190		
Phe	Gln	Leu	Ser	Ser	His	Pro	Ile	Leu	Gly	Asp	Trp	Ser	Ile	Gln	Val
	195						200					205			
Gln	Val	Asn	Asp	Gln	Thr	Tyr	Tyr	Gln	Ser	Phe	Gln	Val	Ser	Glu	Tyr
	210					215					220				
Val	Leu	Pro	Lys	Phe	Glu	Val	Thr	Leu	Gln	Thr	Pro	Leu	Tyr	Cys	Ser
225					230					235					240
Met	Asn	Ser	Lys	His	Leu	Asn	Gly	Thr	Ile	Thr	Ala	Lys	Tyr	Thr	Tyr
				245					250					255	
Gly	Lys	Pro	Val	Lys	Gly	Asp	Val	Thr	Leu	Thr	Phe	Leu	Pro	Leu	Ser
			260					265					270		
Phe	Trp	Gly	Lys	Lys	Lys	Asn	Ile	Thr	Lys	Thr	Phe	Lys	Ile	Asn	Gly
	275						280				285				
Ser	Ala	Asn	Phe	Ser	Phe	Asn	Asp	Glu	Glu	Met	Lys	Asn	Val	Met	Asp
	290					295					300				
Ser	Ser	Asn	Gly	Leu	Ser	Glu	Tyr	Leu	Asp	Leu	Ser	Ser	Pro	Gly	Pro
305					310					315					320
Val	Glu	Ile	Leu	Thr	Thr	Val	Thr	Glu	Ser	Val	Thr	Gly	Ile	Ser	Arg
				325					330					335	
Asn	Val	Ser	Thr	Asn	Val	Phe	Phe	Lys	Gln	His	Asp	Tyr	Ile	Ile	Glu
			340					345					350		
Phe	Phe	Asp	Tyr	Thr	Thr	Val	Leu	Lys	Pro	Ser	Leu	Asn	Phe	Thr	Ala
		355					360					365			
Thr	Val	Lys	Val	Thr	Arg	Ala	Asp	Gly	Asn	Gln	Leu	Thr	Leu	Glu	Glu
	370					375					380				
Arg	Arg	Asn	Asn	Val	Val	Ile	Thr	Val	Thr	Gln	Arg	Asn	Tyr	Thr	Glu
385					390					395					400
Tyr	Trp	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Gln	Lys	Met	Glu	Ala	Val	Gln
				405					410					415	
Lys	Ile	Asn	Tyr	Thr	Val	Pro	Gln	Ser	Gly	Thr	Phe	Lys	Ile	Glu	Phe
			420					425					430		
Pro	Ile	Leu	Glu	Asp	Ser	Ser	Glu	Leu	Gln	Leu	Lys	Ala	Tyr	Phe	Leu
		435					440				445				
Gly	Ser	Lys	Ser	Ser	Met	Ala	Val	His	Ser	Leu	Phe	Lys	Ser	Pro	Ser
						455					460				
Lys	Thr	Tyr	Ile	Gln	Leu	Lys	Thr	Arg	Asp	Glu	Asn	Ile	Lys	Val	Gly
465					470					475					480
Ser	Pro	Phe	Glu	Leu	Val	Val	Ser	Gly	Asn	Lys	Arg	Leu	Lys	Glu	Leu
				485					490					495	
Ser	Tyr	Met	Val	Val	Ser	Arg	Gly	Gln	Leu	Val	Ala	Val	Gly	Lys	Gln
			500					505					510		

Asn	Ser	Thr	Met	Phe	Ser	Leu	Thr	Pro	Glu	Asn	Ser	Trp	Thr	Pro	Lys
		515					520					525			
Ala	Cys	Val	Ile	Val	Tyr	Tyr	Ile	Glu	Asp	Asp	Gly	Glu	Ile	Ile	Ser
		530					535				540				
Asp	Val	Leu	Lys	Ile	Pro	Val	Gln	Leu	Val	Phe	Lys	Asn	Lys	Ile	Lys
545					550					555					560
Leu	Tyr	Trp	Ser	Lys	Val	Lys	Ala	Glu	Pro	Ser	Glu	Lys	Val	Ser	Leu
				565					570						575
Arg	Ile	Ser	Val	Thr	Gln	Pro	Asp	Ser	Ile	Val	Gly	Ile	Val	Ala	Val
			580				585						590		
Asp	Lys	Ser	Val	Asn	Leu	Met	Asn	Ala	Ser	Asn	Asp	Ile	Thr	Met	Glu
		595					600					605			
Asn	Val	Val	His	Glu	Leu	Glu	Leu	Tyr	Asn	Thr	Gly	Tyr	Tyr	Leu	Gly
		610				615					620				
Met	Phe	Met	Asn	Ser	Phe	Ala	Val	Phe	Gln	Glu	Cys	Gly	Leu	Trp	Val
625					630					635					640
Leu	Thr	Asp	Ala	Asn	Leu	Thr	Lys	Asp	Tyr	Ile	Asp	Gly	Val	Tyr	Asp
				645					650						655
Asn	Ala	Glu	Tyr	Ala	Glu	Arg	Phe	Met	Glu	Glu	Asn	Glu	Gly	His	Ile
			660					665					670		
Val	Asp	Ile	His	Asp	Phe	Ser	Leu	Gly	Ser	Ser	Pro	His	Val	Arg	Lys
			675				680					685			
His	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Leu	Asp	Thr	Asn	Met	Gly	Tyr	Arg
		690				695					700				
Ile	Tyr	Gln	Glu	Phe	Glu	Val	Thr	Val	Pro	Asp	Ser	Ile	Thr	Ser	Trp
705					710					715					720
Val	Ala	Thr	Gly	Phe	Val	Ile	Ser	Glu	Asp	Leu	Gly	Leu	Gly	Leu	Thr
				725					730						735
Thr	Thr	Pro	Val	Glu	Leu	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Ile	Phe	Leu
			740					745					750		
Asn	Leu	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Glu	Phe	Ala	Leu	Glu	Ile
		755					760					765			
Thr	Ile	Phe	Asn	Tyr	Leu	Lys	Asp	Ala	Thr	Glu	Val	Lys	Val	Ile	Ile
		770				775					780				
Glu	Lys	Ser	Asp	Lys	Phe	Asp	Ile	Leu	Met	Thr	Ser	Ser	Glu	Ile	Asn
785					790					795					800
Ala	Thr	Gly	His	Gln	Gln	Thr	Leu	Leu	Val	Pro	Ser	Glu	Asp	Gly	Ala
			805						810					815	
Thr	Val	Leu	Phe	Pro	Ile	Arg	Pro	Thr	His	Leu	Gly	Glu	Ile	Pro	Ile
			820					825					830		
Thr	Val	Thr	Ala	Leu	Ser	Pro	Thr	Ala	Ser	Asp	Ala	Val	Thr	Gln	Met
			835				840					845			
Ile	Leu	Val	Lys	Ala	Glu	Gly	Ile	Glu	Lys	Ser	Tyr	Ser	Gln	Ser	Ile
		850				855					860				
Leu	Leu	Asp	Leu												

Tyr Gln Arg Glu Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala
965 970 975
Phe Gly Asn Tyr Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val
980 985 990
Leu Arg Cys Phe Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn
995 1000 1005
Val Leu His Arg Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn
1010 1015 1020
Gly Glu Phe Trp Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly
1025 1030 1035 1040
Gly Asn Lys Ser Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu
1045 1050 1055
Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
1060 1065 1070
His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
1075 1080 1085
Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
1090 1095 1100
Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
1105 1110 1115 1120
Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
1125 1130 1135
Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
1140 1145 1150
Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
1155 1160 1165
Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
1170 1175 1180
Thr Val Ala Leu Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr
1185 1190 1195 1200
Glu Arg Thr Asn Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser
1205 1210 1215
Pro Val Lys Phe Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr
1220 1225 1230
Ala Glu Leu Ala Val Val Gln Pro Met Ala Val Asn Ile Ser Ala Asn
1235 1240 1245
Gly Phe Gly Phe Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys
1250 1255 1260
Ala Ser Gly Ser Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala
1265 1270 1275 1280
Phe Asp Leu Asp Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His
1285 1290 1295
Val Asp Leu Asn Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly
1300 1305 1310
Met Ala Leu Met Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser
1315 1320 1325
Glu Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His
1330 1335 1340
Gly Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys
1345 1350 1355 1360
Val Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp
1365 1370 1375
Ala Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val
1380 1385 1390
Arg Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser
1395 1400 1405

Asp Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His
 1410 1415 1420
 His His Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe
 1425 1430 1435 1440
 Met Glu Leu Trp Leu
 1445

<210> 3
 <211> 4287
 <212> DNA
 <213> homo sapiens

<400> 3
 atgcagggcc caccgctcct gaccgcccgc cacctcctct gcgtgtgcac cgccgcgctg 60
 gccgtggctc ccgggcctcg gtttctgggt acagccccag ggatcatcag gcccgaggga 120
 aatgtgacta ttgggtgga gcttctggaa cactgccctt cacaggtgac tgtgaaggcg 180
 gagctgctca agacagcatc aaacctcact gtctctgtcc tgggaagcaga aggagtcttt 240
 gaaaaaggct cttttaagac acttactctt ccatcactac ctctgaacag tgcagatgag 300
 atttatgagc tacgtgtaac cggacgtacc caggatgaga ttttattctc taatagtacc 360
 cgcttatcat ttgagaccaa gagaatatct gtcttcattc aaacagacaa ggccttatac 420
 aagccaaagc aagaagtga gtttcgcatt gttacactct tctcagattt taagccttac 480
 aaaacctctt taaacattct cattaaggac cccaaatcaa atttgatcca acagtgggtg 540
 tcacaacaaa gtgatcttgg agtcatttcc aaaacttttc agctatcttc ccatccaata 600
 cttgggtgact ggtctattca agttcaagt atgaccaga catattatca atcatttcag 660
 gtttcagaat atgtattacc aaaatttgaa gtgactttgc agacaccatt atattgttct 720
 atgaattcta agcatttaaa tgggtaccatc acggcaaagt atacatatgg gaagccagtg 780
 aaaggagacg taacgcttac atttttacct ttatcctttt ggggaaagaa gaaaaatatt 840
 acaaaaaacat ttaagataaa tggatctgca aacttctctt ttaatgatga agagatgaaa 900
 aatgtaatgg attcttcaaa tggactttct gaatacctgg atctatcttc ccctggacca 960
 gtagaaatth taaccacagt gacagaatca gttacaggta tttcaagaaa tgtaagcact 1020
 aatgtgttct tcaagcaaca tgattacatc attgagtttt ttgattatac tactgtcttg 1080
 aagccatctc tcaacttcac agccactgtg aaggtaactc gtgctgatgg caaccaactg 1140
 actcttgaag aaagaagaaa taatgtatgc ataacagtga cacagagaaa ctatactgag 1200
 tactggagcg gatctaacag tggaaatcag aaaatggaag ctgttcagaa aataaattat 1260
 actgtccccc aaagtggaa ttttaagatt gaattcccaa tcctggagga ttccagtgag 1320
 ctacagttga aggcctatth ccttggtagt aaaagtagca tggcagttca tagtctgttt 1380
 aagtctccta gtaagacata catccaacta aaaacaagag atgaaaatat aaaggtggga 1440
 tcgccttttg agttggtggt tagtggcaac aaacgattga aggagttaag ctatatggta 1500
 gtatccaggg gacagttggt ggctgtagga aaacaaaatt caacaatggt ctctttaaca 1560
 ccagaaaatt cttggactcc aaaagcctgt gtaatttgtt attatatgga agatgatggg 1620
 gaaattataa gtgatgttct aaaaattcct gttcagcttg tttttaaaaa taagataaag 1680
 ctatatggga gtaaagtga agctgaacca tctgagaaag tctctcttag gatctctgtg 1740
 acacagcctg actccatagt tgggattgta gctgttgaca aaagtgtgaa tctgatgaat 1800
 gcctctaatt atattacaat ggaaaatgtg gtccatgagt tggaaacttta taacacagga 1860
 tattatttag gcatgttcat gaattctttt gcagtctttc agaatgtgg actctgggta 1920
 ttgacagatg caaacctcac gaaggattat attgatgggt tttatgacaa tgcagaatat 1980
 gctgagaggt ttatggagga aaatgaagga catattgtag atattcatga cttttctttg 2040
 ggtagcagtc cacatgtccg aaagcatttt ccagagactt ggatttggct agacaccaac 2100
 atgggttaca ggtattacca agaatttgaa gtaactgtac ctgattctat cacttcttgg 2160
 gtggctactg gttttgtgat ctctgaggac ctgggtcttg gactaacaac tactccagtg 2220
 gagctccaag ccttccaacc atttttcatt tttttgaatc ttccctactc tgttatcaga 2280
 ggtgaagaat ttgcttttga aataactata ttcaattatt tgaaagatgc cactgagggt 2340
 aaggtaatca ttgagaaaag tgacaaatth gatattctaa tgacttcaag tgaaataaat 2400
 gccacaggcc accagcagac ctttctgggt cccagtgagg atggggcaac tgttcttttt 2460
 cccatcaggc caacacatct gggagaaatt cctatcacag tcacagctct ttcaccact 2520
 gcttctgatg ctgtcaccca gatgatttth gtaaaggctg aaggaataga aaaatcatat 2580

```

tcacaatoca tcttattaga cttgactgac aataggctac agagtaccct gaaaactttg 2640
agttttctcat ttctctctaa tacagtgact ggcagtgaaa gagttcagat cactgcaatt 2700
ggagatgttc ttggtccttc catcaatggc ttagcctcat tgattcggat gccttatggc 2760
tgtggtgaac agaacatgat aaattttgct ccaaataattt acattttgga ttatctgact 2820
aaaaagaaac aactgacaga taatttgaaa gaaaaagctc tttcatttat gagggcaagg 2880
taccagagag aacttctcta tcagagggaa gatggctcct tcagtgtctt tgggaattat 2940
gacccttctg ggagcacttg gttgtcagct tttgttttaa gatgtttcct tgaagccgat 3000
ccttacatag atattgatca gaatgtgtta cacagaacat acacttggct taaaggacat 3060
cagaaatcca acggtgaatt ttgggatcca ggaagagtga ttcatagtga gcttcaagg 3120
ggcaataaaa gtccagtaac acttacagcc tatattgtaa cttctctcct gggatataga 3180
aagtatcagc ctaacattga tgtgcaagag tctatccatt ttttggagtc tgaattcagt 3240
agaggaattt cagacaatta tactctagcc cttataactt atgcattgtc atcagtgggg 3300
agtcctaaag cgaaggaagc tttgaatatg ctgacttgga gagcagaaca agaaggtggc 3360
atgcaattct ggggtgtcatc agagtccaaa ctttctgact cctggcagcc acgctccctg 3420
gatattgaag ttgcagccta tgcactgctc tcacacttct tacaatttca gacttctgag 3480
ggaatcccaa ttatgaggtg gctaagcagg caaagaaata gcttgggtgg ttttgcactc 3540
actcaggata ccactgtggc tttaaaggct ctgtctgaat ttgcagccct aatgaatata 3600
gaaaggacaa atatccaagt gaccgtgacg ggccttagct caccaagtc tcttgctgtg 3660
gtacagccaa tggcagttaa tatttccgca aatgggtttt gatttgctat ttgtcagctc 3720
aatgttgtat ataattgtga ggcttctggg tcttctagaa gacgaagatc tatccaaaat 3780
caagaagcct ttgatttaga tgttgctgta aaagaaaata aagatgatct caatcatgtg 3840
gatttgaatg tgtgtacaag cttttcgggc ccgggtagga gtggcatggc tcttatggaa 3900
gttaacctat taagtggctt tatggtgctc tcagaagcaa tttctctgag cgagacagt 3960
aagaaagtgg aatatgatca tggaaaactc aacctctatt tagattctgt aaatgaaacc 4020
cagttttgtg ttaatatcc tgctgtgaga aactttaaag tttcaaatac ccaagatgct 4080
tcagtgtcca tagtggatta ctatgagcca aggagacagg cggtgagaag ttacaactct 4140
gaagtgaagc tgtcctcctg tgacctttgc agtgatgtcc agggctgccg tccttgtgag 4200
gatggagctt caggctccca tcatcactct tcagtcattt ttattttctg tttcaagctt 4260
ctgtacttta tggaactttg gctgtga 4287

```

```

<210> 4
<211> 1428
<212> PRT
<213> homo sapiens

```

```

<400> 4
Met Gln Gly Pro Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys
1 5 10 15
Thr Ala Ala Leu Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala
20 25 30
Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
35 40 45
Leu Glu His Cys Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys
50 55 60
Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
65 70 75 80
Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
85 90 95
Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
100 105 110
Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
115 120 125
Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
130 135 140
Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
145 150 155 160

```

Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
 165 170 175
 Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr
 180 185 190
 Phe Gln Leu Ser Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val
 195 200 205
 Gln Val Asn Asp Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr
 210 215 220
 Val Leu Pro Lys Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser
 225 230 235 240
 Met Asn Ser Lys His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr
 245 250 255
 Gly Lys Pro Val Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser
 260 265 270
 Phe Trp Gly Lys Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly
 275 280 285
 Ser Ala Asn Phe Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp
 290 295 300
 Ser Ser Asn Gly Leu Ser Glu Tyr Leu Asp Leu Ser Ser Pro Gly Pro
 305 310 315 320
 Val Glu Ile Leu Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg
 325 330 335
 Asn Val Ser Thr Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu
 340 345 350
 Phe Phe Asp Tyr Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala
 355 360 365
 Thr Val Lys Val Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu
 370 375 380
 Arg Arg Asn Asn Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu
 385 390 395 400
 Tyr Trp Ser Gly Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln
 405 410 415
 Lys Ile Asn Tyr Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe
 420 425 430
 Pro Ile Leu Glu Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu
 435 440 445
 Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser
 450 455 460
 Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
 465 470 475 480
 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu
 485 490 495
 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
 500 505 510
 Asn Ser Thr Met Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys
 515 520 525
 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
 530 535 540
 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
 545 550 555 560
 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu
 565 570 575
 Arg Ile Ser Val Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val
 580 585 590
 Asp Lys Ser Val Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu
 595 600 605

Asn Val Val His Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly	610	615	620
Met Phe Met Asn Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val	625	630	635
Leu Thr Asp Ala Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp	645	650	655
Asn Ala Glu Tyr Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile	660	665	670
Val Asp Ile His Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys	675	680	685
His Phe Pro Glu Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Tyr Arg	690	695	700
Ile Tyr Gln Glu Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp	705	710	715
Val Ala Thr Gly Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr	725	730	735
Thr Thr Pro Val Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu	740	745	750
Asn Leu Pro Tyr Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile	755	760	765
Thr Ile Phe Asn Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile	770	775	780
Glu Lys Ser Asp Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn	785	790	795
Ala Thr Gly His Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala	805	810	815
Thr Val Leu Phe Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile	820	825	830
Thr Val Thr Ala Leu Ser Pro Thr Ala Ser Asp Ala Val Thr Gln Met	835	840	845
Ile Leu Val Lys Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile	850	855	860
Leu Leu Asp Leu Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu	865	870	875
Ser Phe Ser Phe Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln	885	890	895
Ile Thr Ala Ile Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala	900	905	910
Ser Leu Ile Arg Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn	915	920	925
Phe Ala Pro Asn Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln	930	935	940
Leu Thr Asp Asn Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly	945	950	955
Tyr Gln Arg Glu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala	965	970	975
Phe Gly Asn Tyr Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val	980	985	990
Leu Arg Cys Phe Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn	995	1000	1005
Val Leu His Arg Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn	1010	1015	1020
Gly Glu Phe Trp Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly	1025	1030	1035
Gly Asn Lys Ser Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu	1045	1050	1055

Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
 1060 1065 1070
 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
 1075 1080 1085
 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
 1090 1095 1100
 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
 1105 1110 1115 1120
 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
 1125 1130 1135
 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
 1140 1145 1150
 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
 1155 1160 1165
 Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
 1170 1175 1180
 Thr Val Ala Leu Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr
 1185 1190 1195 1200
 Glu Arg Thr Asn Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser
 1205 1210 1215
 Pro Leu Ala Val Val Gln Pro Met Ala Val Asn Ile Ser Ala Asn Gly
 1220 1225 1230
 Phe Gly Phe Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys Ala
 1235 1240 1245
 Ser Gly Ser Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala Phe
 1250 1255 1260
 Asp Leu Asp Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His Val
 1265 1270 1275 1280
 Asp Leu Asn Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly Met
 1285 1290 1295
 Ala Leu Met Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser Glu
 1300 1305 1310
 Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His Gly
 1315 1320 1325
 Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys Val
 1330 1335 1340
 Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp Ala
 1345 1350 1355 1360
 Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val Arg
 1365 1370 1375
 Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser Asp
 1380 1385 1390
 Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His His
 1395 1400 1405
 His Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe Met
 1410 1415 1420
 Glu Leu Trp Leu
 1425

<210> 5

<211> 4903

<212> DNA

<213> homo sapiens

<400> 5

ggaggggtgg agcctccaag tcctgtctca atttagatct ctactctgc tgtaggcgc

60

gcccatttca	gattactaaa	ctcgaattaa	gagggaaaaa	aatatcaggga	ggaggtggca	120
agccacaccc	cacggtgccc	gcgaacttcc	ccggcaacgg	actgtagccc	aggcagacgc	180
cgtccccatt	tcaggtgtcg	taagcttgaa	ttcaataact	ataacggtcc	taaggtagcg	240
aagcgagatg	cagggccccac	cgctcctgac	cgccgccccac	ctcctctgcg	tgtgcaccgc	300
cgcgctggcc	gtggctccccg	ggcctcgggt	tctggtgaca	gccccaggga	tcatacaggcc	360
cggaggaaat	gtgactattg	gggtggagct	tctggaacac	tgcccttcac	aggtgactgt	420
gaaggcggag	ctgctcaaga	cagcatcaaa	cctcactgtc	tctgtcctgg	aagcagaagg	480
agtctttgaa	aaaggctctt	ttaagacact	tactcttcca	tcactacctc	tgaacagtgc	540
agatgagatt	tatgagctac	gtgtaaccgg	acgtaccagg	gatgagattt	tattctctaa	600
tagtaccggc	ttatcatttg	agaccaagag	aatatctgtc	ttcattcaaa	cagacaaggc	660
cttatacaag	ccaaagcaag	aagtgaagtt	tcgcattggt	acactcttct	cagattttta	720
gccttacaaa	acctctttta	acattctcat	taaggacccc	aatcaaatt	tgatccaaca	780
gtggttgtca	caacaagtgt	atcttggagt	catttccaaa	acttttcagc	tatcttccca	840
tccaatactt	gccttagtgt	ctattcgaag	tcaagtgaat	gaccagacat	attatcaatc	900
atttcagggt	tcagaatatg	tattaccaaa	atttgaagtg	actttgcaga	caccattata	960
ttgttctatg	aattctaagc	atttaaattgg	taccatcacg	ccaaagtata	cattatgggaa	1020
gccagtgaag	ggagacgtaa	cgcttacatt	tttaccttta	tccttttggg	gaaagaagaa	1080
aaatattaca	aaaacattta	agataaatgg	atctgcaaac	ttctctttta	atgatgaaga	1140
gatgaaaaat	gtaatggatt	cttcaaattgg	actttctgaa	tacctggatc	tatcttcccc	1200
tggaccagta	gaaattttta	ccacagtgc	agaatcagtt	acaggatatt	caagaaatgt	1260
aagcactaat	gtgttcttca	agcaacatga	ttacatcatt	gagttttttg	attatactac	1320
tgtcttgaag	ccatctctca	acttcacagc	cactgtgaag	gtaactcgtg	ctgatggcaa	1380
ccaactgact	cttgaagaaa	gaagaaataa	tgtagtcata	acagtgcac	agagaaacta	1440
tactgagtac	tggagcggat	ctaacagtgg	aatcagaaa	atggaagctg	ttcagaaaat	1500
aaattatact	gtccccaaa	gtggaacttt	taagattgaa	ttcccaatcc	tggaggattc	1560
cagtgagcta	cagttgaagg	cctatttccct	tggtagttaa	agtagcatgg	cagttcatag	1620
tctgtttaag	tctctagta	agacatacat	ccaactaaaa	acaagagatg	aaaatataaa	1680
ggtgggatcg	ccttttgagt	tgggtggttag	tggcaacaaa	cgattgaagg	agttaaagta	1740
tatggtagta	tccagggggac	agttggtggc	tgtaggaaaa	caaaattcaa	caatgttctc	1800
tttaacacca	gaaaattctt	ggactccaaa	agcctgtgta	attgtgtatt	atattgaaga	1860
tgatggggaa	attataagtg	atgtttctaaa	aattcctgtt	cagcttgttt	ttaaaaataa	1920
gataaagcta	tattggagta	aagtgaagc	tgaaccatct	gagaaagtct	ctcttaggat	1980
ctctgtgaca	cagcctgact	ccatagttgg	gattgtagct	gttgacaaaa	gtgtgaatct	2040
gatgaatgcc	tctaatagata	ttacaatgga	aatgtggtc	catgagttgg	aactttataa	2100
cacaggatat	tatttaggca	tgttcatgaa	ttcttttgca	gtctttcagg	aatgtggact	2160
ctgggtattg	acagatgcaa	acctcacgaa	ggattatatt	gatgggtgtt	atgacaatgc	2220
agaatatgct	gagaggttta	tggaggaaaa	tgaaggacat	attgtagata	ttcatgactt	2280
ttctttgggt	agcagtcac	atgtccgaaa	gcattttcca	gagacttgga	tttggctaga	2340
caccaacatg	ggttacagga	tttaccagaa	atttgaagta	actgtacctg	attctatcac	2400
ttcttgggtg	gctactgggt	ttgtgactct	tgaggacctg	ggtcttggac	taacaactac	2460
tccagtggag	ctccaagcct	tccaaccatt	ttcatttttt	tgaatcttc	cctactctgt	2520
tatcagaggt	gaagaatttg	ctttggaaat	aactatatct	aattatttga	aagatgccac	2580
tgagggttaag	gtaatcattg	agaaaagtga	caaatattgat	attctaata	cttcaagtga	2640
aataaatgcc	acaggccacc	agcagaccct	tctggttccc	agtgaggatg	gggcaactgt	2700
tctttttccc	atcaggccaa	cacatctggg	agaaattcct	atcacagtca	cagctctttc	2760
accactgct	tctgatgctg	tcaccagat	gatttttagta	aaggctgaag	gaatagaaaa	2820
atcatattca	caatccatct	tattagactt	gactgacaat	aggctacaga	gtaccctgaa	2880
aactttgagt	ttctcatttc	ctcctaatac	agtgactggc	agtgaagag	ttcagatcac	2940
tgcaattgga	gatgttcttg	gtccttccat	caatggctta	gcctcattga	ttcggatgcc	3000
ttatggctgt	ggtgaacaga	acatgataaa	ttttgctcca	aatattttaca	ttttggatta	3060
tctgactaag	aagaacaac	tgacagataa	tttgaaagaa	aaagctcttt	catttatgag	3120
gcaagggttac	cagagagaac	ttctctatca	gagggaagat	ggctctttca	gtgcttttgg	3180
gaattatgac	ccttctggga	gcacttgggt	gtcagctttt	gttttaagat	gtttccttga	3240
agccgatcct	tacatagata	ttgatcagaa	tgtgttacac	agaacataca	cttggcttaa	3300
aggacatcag	aatccaacg	gtgaattttg	ggatccagga	agagtgatcc	atagttagct	3360
tcaagggtggc	aataaaagtc	cagtaacact	tacagcctat	attgtaaact	ctctcctggg	3420

atatagaaag	tatcagccta	acattgatgt	gcaagagtct	atccattttt	tggagtctga	3480
attcagtaga	ggaatttcag	acaattatac	tctagccctt	ataacttatg	cattgtcatc	3540
agtggggagt	cctaaagcga	aggaagcttt	gaatatgctg	acttggagag	cagaacaaga	3600
aggtggcatg	caattctggg	tgtcatcaga	gtccaaactt	tctgactcct	ggcagccacg	3660
ctccctggat	attgaagttg	cagcctatgc	actgctctca	cacttcttac	aatttcagac	3720
ttctgaggga	atcccaatta	tgagggtggt	aagcaggcaa	agaaatagct	tgggtgggtt	3780
tgcacttact	caggatacca	ctgtggcttt	aaaggctctg	tctgaatttg	cagcccta	3840
gaatacagaa	aggacaaata	tccaagtgac	cgtgacgggg	cctagctcac	caagtctgt	3900
aaagtttctg	attgacacac	acaaccgctt	actccttcag	acagcagagc	ttgctgtggt	3960
acagccaatg	gcagttaata	tttccgcaaa	tggttttgga	tttgctat	gtcagctcaa	4020
tgttgatat	aatgtgaagg	cttctgggtc	ttctagaaga	cgaagatcta	tccaaaatca	4080
agaagccttt	gatttagatg	ttgctgtaaa	agaaaataaa	gatgatctca	atcatgtgga	4140
tttgaatgtg	tgtacaagct	tttcgggccc	gggtaggagt	ggcatggctc	ttatggaagt	4200
taacctatta	agtggcttta	tgggtgcctt	agaagcaatt	tctctgagcg	agacagtgaa	4260
gaaagtggaa	tatgatcatg	gaaaactcaa	cctctattta	gattctgtaa	atgaaaccca	4320
gttttgtggt	aatattcctg	ctgtgagaaa	ctttaaagtt	tcaaataccc	aagatgcttc	4380
agtgtccata	gtggattact	atgagccaag	gagacaggcg	gtgagaagtt	acaactctga	4440
agtgaagctg	tcctcctgtg	acctttgcag	tgatgtccag	ggctgccgtc	cttgtgagga	4500
tggagcttca	ggctcccatc	atcactcttc	agtcattttt	attttctgtt	tcaagcttct	4560
gtactttatg	gaactttggc	tgtgatttat	ttttaaagga	ctctgtgtaa	cactaacatt	4620
tccagtagtc	acatgtgatt	gttttgtttt	cgtagaagaa	tactgcttct	attttgaaaa	4680
aagagttttt	tttctttcta	tgggggttgc	gggatgggtg	acaacaggtc	ctagcatgta	4740
tagctgcata	gatttcttca	cctgatcttt	gtgtggaaga	tcagaatgaa	tgcagttgtg	4800
tgtctatatt	ttcccctctc	aaaatctttt	agaatttttt	tggaggtggt	tgttttctcc	4860
agaataaagg	tattacttta	gaaaaaaaaa	aaaaaaaaaa	aaa		4903